

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/517,155A
Source: JFWP
Date Processed by STIC: 08/14/2006

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/517,155A

DATE: 08/14/2006
TIME: 13:25:45

Input Set : A:\211080011U6.TXT
Output Set: N:\CRF4\08142006\J517155A.raw

4 <110> APPLICANT: Chang, Chawnshang
 6 <120> TITLE OF INVENTION: Androgen Receptor Coregulators
 9 <130> FILE REFERENCE: 21108.0011U6
 11 <140> CURRENT APPLICATION NUMBER: 10/517,155A
 C--> 12 <141> CURRENT FILING DATE: 2004-12-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/17937
 15 <151> PRIOR FILING DATE: 2003-06-06
 17 <150> PRIOR APPLICATION NUMBER: US 60/387,087
 18 <151> PRIOR FILING DATE: 2002-06-06
 20 <160> NUMBER OF SEQ ID NOS: 47
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1721
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapien
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (40)...(1464)
 33 <220> FEATURE:
 34 <221> NAME/KEY: misc_feature
 35 <222> LOCATION: (1120)...(1452)
 36 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
 37 C-terminal domain
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_feature
 41 <222> LOCATION: (697)...(834)
 42 <223> OTHER INFORMATION: Coding sequence and polypeptide region which may
 43 form a cystein-rich RING finger motif
 45 <220> FEATURE:
 46 <221> NAME/KEY: misc_feature
 47 <222> LOCATION: (964)...(1089)
 48 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
 49 cystein-rich B box like structure
 51 <400> SEQUENCE: 1
 52 ggtctctggc ctccctctc tgagcactct gaggtcctt atg tcg tca gaa gat 54
 53 Met Ser Ser Glu Asp
 54 1 5
 55 cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat
 56 Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp 102
 57 10 15 20
 58 gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg 150
 59 Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
 60 25 30 35

(Pg 6)

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64 atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat	198
65 Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn	
66 40 45 50	
68 tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt	246
69 Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe	
70 55 60 65	
72 ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc	294
73 Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser	
74 70 75 80 85	
76 tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act	342
77 Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr	
78 90 95 100	
80 cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac	390
81 Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His	
82 105 110 115	
84 cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag	438
85 Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu	
86 120 125 130	
88 acc cta gca tac ttg aat att gtc tct ctt gag ctc aag att ggt	486
89 Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly	
90 135 140 145	
92 tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca	534
93 Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr	
94 150 155 160 165	
96 gag cta gat ttt gga gga gct gct gta gac caa gag gaa	582
97 Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu	
98 170 175 180	
100 att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg	630
101 Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu	
102 185 190 195	
104 atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt	678
105 Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe	
106 200 205 210	
108 aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgc gag aag ctg ggt	726
109 Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly	
110 215 220 225	
112 agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc	774
113 Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala	
114 230 235 240 245	
116 tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa	822
117 Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln	
118 250 255 260	
120 tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt	870
121 Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly	
122 265 270 275	
124 cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc	918
125 Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg	
126 280 285 290	
128 ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc	966

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129	Leu	Leu	Leu	Gln	Ser	Ser	Leu	Asp	Leu	Met	Ala	Asp	Val	Val	Tyr	Cys	
130	295						300						305				
132	ccc	cgg	ccg	tgc	tgc	cag	ctg	cct	gtg	atg	cag	gaa	cct	ggc	tgc	acc	1014
133	Pro	Arg	Pro	Cys	Cys	Gln	Leu	Pro	Val	Met	Gln	Glu	Pro	Gly	Cys	Thr	
134	310						315				320					325	
136	atg	ggt	atc	tgc	tcc	agc	tgc	aat	ttt	gcc	ttc	tgt	act	ttg	tgc	agg	1062
137	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe	Cys	Thr	Leu	Cys	Arg	
138							330				335					340	
140	ttg	acc	tac	cat	ggg	gtc	tcc	cca	tgt	aag	gtg	act	gca	gag	aaa	tta	1110
141	Leu	Thr	Tyr	His	Gly	Val	Ser	Pro	Cys	Lys	Val	Thr	Ala	Glu	Lys	Leu	
142							345				350					355	
144	atg	gac	tta	cga	aat	gaa	tac	ctg	caa	gcg	gat	gag	gct	aat	aaa	aga	1158
145	Met	Asp	Leu	Arg	Asn	Glu	Tyr	Leu	Gln	Ala	Asp	Glu	Ala	Asn	Lys	Arg	
146							360				365					370	
148	ctt	ttg	gat	caa	agg	tat	ggt	aag	aga	gtg	att	cag	aag	gca	ctg	gaa	1206
149	Leu	Leu	Asp	Gln	Arg	Tyr	Gly	Lys	Arg	Val	Ile	Gln	Lys	Ala	Leu	Glu	
150							375				380					385	
152	gag	atg	gaa	agt	aag	gag	tgg	cta	gag	aag	aac	tca	aag	agc	tgc	cca	1254
153	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn	Ser	Lys	Ser	Cys	Pro	
154	390						395				400					405	
156	tgt	tgt	gga	act	ccc	ata	gag	aaa	tta	gac	gga	tgt	aac	aag	atg	aca	1302
157	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly	Cys	Asn	Lys	Met	Thr	
158							410				415					420	
160	tgt	act	ggc	tgt	atg	caa	tat	ttc	tgt	tgg	att	tgc	atg	ggt	tct	ctc	1350
161	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile	Cys	Met	Gly	Ser	Leu	
162							425				430					435	
164	tct	aga	gca	aac	cct	tac	aaa	cat	ttc	aat	gac	cct	ggt	tca	cca	tgt	1398
165	Ser	Arg	Ala	Asn	Pro	Tyr	Lys	His	Phe	Asn	Asp	Pro	Gly	Ser	Pro	Cys	
166							440				445					450	
168	ttt	aac	cgg	ctg	ttt	tat	gct	gtg	gat	gtt	gac	gac	gat	att	tgg	gaa	1446
169	Phe	Asn	Arg	Leu	Phe	Tyr	Ala	Val	Asp	Val	Asp	Asp	Asp	Ile	Trp	Glu	
170							455				460					465	
172	gat	gag	gta	gaa	gac	tag	ttaactactg	ctcaagatat	ttaactactg								1494
173	Asp	Glu	Val	Glu	Asp	*											
174	470																
176	ctcaagatat	ggaagtggat	tgttttccc	taatcttcg	tcaagtacac	aaagtaactt											1554
177	tgcggatat	ttagggtact	attcattcac	tcttcctgcg	tagaagatat	ggaagaacga											1614
178	ggttatatt	ttcatgttgt	actactgaag	aaggtgcatt	gatacattt	taaatgtaa											1674
179	ttgagaaaaa	tttataagcc	aaaggttcag	aaaattaaac	tacagaa												1721
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182	<211>	LENGTH:	474														
183	<212>	TYPE:	PRT														
184	<213>	ORGANISM:	Homo sapien														
186	<400>	SEQUENCE:	2														
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188	1				5					10					15		
189	Ala	Ser	Ile	Tyr	Asp	Gly	Asp	Glu	Phe	Arg	Lys	Ala	Glu	Ser	Val	Gln	
190							20				25					30	
191	Gly	Gly	Glu	Thr	Arg	Ile	Tyr	Leu	Asp	Leu	Pro	Gln	Asn	Phe	Lys	Ile	

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192	35	40	45	
193	Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu			
194	50	55	60	
195	Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro			
196	65	70	75	80
197	Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys			
198	85	90	95	
199	Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn			
200	100	105	110	
201	Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln			
202	115	120	125	
203	Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe			
204	130	135	140	
205	Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln			
206	145	150	155	160
207	Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp			
208	165	170	175	
209	Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu			
210	180	185	190	
211	Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln			
212	195	200	205	
213	Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe			
214	210	215	220	
215	Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His			
216	225	230	235	240
217	Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg			
218	245	250	255	
219	Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser			
220	260	265	270	
221	Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe			
222	275	280	285	
223	Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala			
224	290	295	300	
225	Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln			
226	305	310	315	320
227	Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe			
228	325	330	335	
229	Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val			
230	340	345	350	
231	Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp			
232	355	360	365	
233	Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile			
234	370	375	380	
235	Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn			
236	385	390	395	400
237	Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly			
238	405	410	415	
239	Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile			
240	420	425	430	

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241 Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
242 435 440 445
243 Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
244 450 455 460
245 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
246 465 470
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1335
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapien
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)...(1335)
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (750)...(1332)
260 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
261 C-terminal binding domain
263 <220> FEATURE:
264 <221> NAME/KEY: misc_feature
265 <222> LOCATION: (631)...(783)
266 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
267 cystein rich LIM motif
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (808)...(996)
272 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
273 cystein rich LIM motif
275 <220> FEATURE:
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: (985)...(1137)
278 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
279 cystein rich LIM motif
281 <220> FEATURE:
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: (1162)...(1314)
284 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
285 cystein rich LIM motif
287 <400> SEQUENCE: 3
288 atg cca agg tca ggg gct ccc aaa gag cgc cct gcg gag cct ctc acc 48
289 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
290 1 5 10 15
292 cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct 96
293 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
294 20 25 30
296 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag
297 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys 144
298 35 40 45
300 cct cgg tcc cca aag cct gca gcc ccg gcc cct cca ttc tcc tct 192

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/14/2006
PATENT APPLICATION: US/10/517,155A TIME: 13:25:46

Input Set : A:\211080011U6.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,15,17,18,20,21,23,24,25,26,27
Seq#:11; Xaa Pos. 28,30,31
Seq#:12; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23,25
Seq#:12; Xaa Pos. 26,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:12; Xaa Pos. 48,49

VERIFICATION SUMMARY**PATENT APPLICATION: US/10/517,155A****DATE: 08/14/2006****TIME: 13:25:46****Input Set : A:\211080011U6.TXT****Output Set: N:\CRF4\08142006\J517155A.raw**

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

M:341 Repeated in SeqNo=11

L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

M:341 Repeated in SeqNo=12